GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2004, 14:48:54 ; Search time 23 Seconds
(without alignments)
2062.794 Million cell updates/sec

Title: US-10-063-579-70
Perfect score: 4791
Sequence: 1 MGLFRGFVFLLVLCLLHQSN.....LVLSVIGSVVIVNFILSTTI 919

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4760	99.4	917	4	US-09-049-698-41	Sequence 41, Appl
2	2879.5	60.1	914	4	US-09-193-562D-28	Sequence 28, Appl
3	2879.5	60.1	914	4	US-09-623-624-6	Sequence 6, Appli
4	2681	56.0	913	4	US-09-623-624-2	Sequence 2, Appli
5	2431.5	50.8	903	4	US-09-193-562D-46	Sequence 46, Appl
6	2426.5	50.6	903	4	US-09-623-624-18	Sequence 18, Appl
7	2338.5	48.8	905	4	US-09-193-562D-2	Sequence 2, Appli
8	2278	47.5	902	4	US-09-193-562D-34	Sequence 34, Appl
9	2176.5	45.4	1000	4	US-09-193-562D-30	Sequence 30, Appl
10	2103.5	43.9	795	4	US-09-193-562D-11	Sequence 11, Appl
11	2103.5	43.9	821	4	US-09-193-562D-12	Sequence 12, Appl
12	1950.5	40.7	943	4	US-09-643-597-161	Sequence 161, App
13	1950.5	40.7	943	4	US-09-480-884A-161	Sequence 161, App
14	1950.5	40.7	943	4	US-09-542-615A-161	Sequence 161, App
15	1950.5	40.7	943	4	US-09-606-421B-161	Sequence 161, App
16	1950.5	40.7	943	4	US-09-623-624-4	Sequence 4, Appli
17	1950.5	40.7	943	4	US-09-221-107-161	Sequence 161, App
18	1950	40.7	920	4	US-09-643-597-357	Sequence 357, App
19	1948.5	40.7	943	4	US-09-193-562D-32	Sequence 32, Appl
20	1913	39.9	942	4	US-09-919-172-87	Sequence 87, Appl
21	1706	35.6	791	4	US-09-643-597-170	Sequence 170, App
22	1706	35.6	791	4	US-09-480-884A-170	Sequence 170, App
23	1706	35.6	791	4	US-09-542-615A-170	Sequence 170, App
24	1706	35.6	791	4	US-09-606-421B-170	Sequence 170, App
25	1275	26.6	592	4	US-09-643-597-169	Sequence 169, App
26	1275	26.6	592	4	US-09-480-884A-169	Sequence 169, App
27	1275	26.6	592	4	US-09-542-615A-169	Sequence 169, App
28	1275	26.6	592	4	US-09-606-421B-169	Sequence 169, App
29	987.5	20.6	342	4	US-09-193-562D-13	Sequence 13, Appl
30	693.5	14.5	228	1	US-08-469-667-9	Sequence 9, Appli
31	693.5	14.5	228	4	US-09-224-110-9	Sequence 9, Appli
32	693.5	14.5	228	5	PCT-US95-07289-9	Sequence 9, Appli
33	468	9.8	203	4	US-09-193-562D-3	Sequence 3, Appli
34	218	4.6	40	4	US-09-049-698-45	Sequence 45, Appl
35	174.5	3.6	1541	3	US-08-296-791-3	Sequence 3, Appli
36	174.5	3.6	1541	4	US-09-839-996-3	Sequence 3, Appli
37	174.5	3.6	1541	4	US-10-080-505-3	Sequence 3, Appli
38	174.5	3.6	1541	5	PCT-US95-10661A-3	Sequence 3, Appli
39	167	3.5	31	4	US-09-049-698-43	Sequence 43, Appl
40	157.5	3.3	1702	3	US-08-296-791-5	Sequence 5, Appli
41	157.5	3.3	1702	4	US-09-839-996-5	Sequence 5, Appli
42	157.5	3.3	1702	4	US-10-080-505-5	Sequence 5, Appli
43	157.5	3.3	1702	5	PCT-US95-10661A-5	Sequence 5, Appli
44	151	3.2	1612	1	US-08-169-927-2	Sequence 2, Appli
45	150	3.1	1426	3	US-09-136-574A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-049-698-41
; Sequence 41, Application US/09049698
; Patent No. 6368792
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA A.
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
; TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,856
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6068.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 917 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: No. 6368792e
US-09-049-698-41

Query Match 99.4%; Score 4760; DB 4; Length 917;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 916; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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Qy    1 MGLFRGFVFLLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTAS 60
Db    1 MGLFRGFVFLLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTAS 60

Qy   61 TYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQ 120
Db   61 TYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQ 120

Qy  121 FTECGEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSK 180
Db  121 FTECGEKGEYIHFTPDLLLEKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSK 180

Qy  181 KIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFM 240
Db  181 KIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFM 240

Qy  241 QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLL 300
Db  241 QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLL 300

Qy  301 KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKLI 360
Db  301 KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKLI 360

Qy  361 QIKSSDERNTLMAGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTAS 420
Db  361 QIKSSDERNTLMAGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTAS 420

Qy  421 SCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGN 480
Db  421 SCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGN 480

Qy  481 TDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIM 540
Db  481 TDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIM 540

Qy  541 ENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM 600
Db  541 ENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM 600

Qy  601 NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGV 660
Db  601 NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGV 660

Qy  661 YSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEID 720
Db  661 YSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEID 720

Qy  721 EDTQTTLEDFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIILTWTAPGDN 780
Db  721 EDTQTTLEDFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIILTWTAPGDN 780

Qy  781 FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATH 840
Db  781 FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATH 840

Qy  841 IFIAIKSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL 900
Db  841 IFIAIKSIDKSNLTSKVSNIAQVTLFIPQANPDDID--PTPTPTPTPDKSHNSGVNISTL 898

Qy  901 VLSVIGSVVIVNFILSTTI 919
Db  899 VLSVIGSVVIVNFILSTTI 917
```

RESULT 2
US-09-193-562D-28
; Sequence 28, Application US/09193562D
; Patent No. 6309857
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-562D-28

Query Match 60.1%; Score 2879.5; DB 4; Length 914;
Best Local Similarity 61.6%; Pred. No. 8.3e-248;
Matches 563; Conservative 124; Mismatches 216; Indels 11; Gaps 8;

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Qy    1 MGLFRGFVFLLVLCLLHQS-NTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTA 59
Db    1 MGPFKSSVFILILHLLEGALSNSLIQLNNNGYEGIVVAIDPNVPEDETLIQQIKDMVTQA 60

Qy   60 STYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTK 119
Db   61 SLYLFEATGKRFYFKNVAILIPETWKTKADYVRPKLETYKNADVLVAESTPPGNDEPYTE 120

Qy  120 QFTECGEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKS 179
Db  121 QMGNCGEKGERIHLTPDFIAGKKLAEYGPQGKAFVHEWAHLRWGVFDEYNNDEKFYLSNG 180

Qy  180 KKIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMF 239
Db  181 -RIQAVRCSAGITGTNVVKKCQGGSCYTKRCTFNKVTGLYEKGCEFVLQSRQTEKASIMF 239

Qy  240 MQSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSL 299
Db  240 AQHVDSIVEFCTEQNHNKEAPNKQNQKCNLRSTWEVIRDSEDFKKTTPMTTQPPNPTFSL 299

Qy  300 LKISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKL 359
Db  300 LQIGQRIVCLVLDKSGSMATGNRLNRLNQAGQLFLLQTVELGSWVGMVTFDSAAHVQSEL 359

Qy  360 IQIKSSDERNTLMAGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTA 419
Db  360 IQINSGSDRDTLAKRLPAAASGGTSICSGLRSAFTVIRKKY-PTDGSEIVLLTDGEDNTI 418

Qy  420 SSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSG 479
Db  419 SGCFNEVKQSGAIIHTVALGPSAAQELEELSKMTGGLQTYASDQVQNNGLIDAFGALSSG 478

Qy  480 NTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTI 539
Db  479 NGAVSQRSIQLESKGLTLQNSQWMNGTVIVDSTVGKDTLFLITWTTQPPQILLWDPSGQK 538

Qy  540 MENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAK 599
Db  539 QGGFVVDKNTKMAYLQIPGIAKVGTWKYSLQASS--QTLTLTVTSRASNATLPPITVTSK 596

Qy  600 MNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDG 659
Db  597 TNKDTSKFPSPLVVYANIRQGASPILRASVTALIESVNGKTVTLQLLDNGAGADATKDDG 656

Qy  660 VYSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEI 719
Db  657 VYSRYFTTYDTNGRYSVKVRALGGVNAARRRVIPQQSGALYIPGWIENDEIQWNPPRPEI 716

Qy  720 D-EDTQTTLEDFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKII-LTWTAP 777
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2004, 14:43:13 ; Search time 50 Seconds
(without alignments)
5799.225 Million cell updates/sec

Title: US-10-063-579-70
Perfect score: 4791
Sequence: 1 MGLFRGFVFLLVLCLLHQSN.....LVLSVIGSVVIVNFILSTTI 919

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4763	99.4	917	4	Q9UNF7	Q9unf7 homo sapien
2	2884.5	60.2	914	4	Q9UPC6	Q9upc6 homo sapien
3	2882.5	60.2	914	4	O95151	O95151 homo sapien
4	2879.5	60.1	914	4	Q9UNF6	Q9unf6 homo sapien
5	2765	57.7	917	6	Q9TUB5	Q9tub5 sus scrofa
6	2681	56.0	913	11	Q9D7Z6	Q9d7z6 mus musculu
7	2677	55.9	913	11	Q8R049	Q8r049 mus musculu
8	2396	50.0	469	4	Q9NXP1	Q9nxp1 homo sapien
9	2343.5	48.9	909	11	Q91ZF5	Q91zf5 mus musculu
10	2343	48.9	902	11	Q9EQR4	Q9eqr4 mus musculu
11	2341.5	48.9	905	6	O18741	O18741 bos taurus
12	2333	48.7	902	11	Q9R070	Q9r070 mus musculu
13	2332	48.7	902	11	Q9QX15	Q9qx15 mus musculu
14	2331	48.7	902	11	Q8C324	Q8c324 mus musculu
15	2324	48.5	902	11	Q8CCM1	Q8ccm1 mus musculu
16	2319.5	48.4	901	11	O88860	O88860 mus musculu
17	2107	44.0	820	6	O18743	O18743 bos taurus
18	2104.5	43.9	794	6	O18742	O18742 bos taurus
19	1950.5	40.7	943	4	Q9Y6N2	Q9y6n2 homo sapien
20	1941.5	40.5	943	4	Q9UQC9	Q9uqc9 homo sapien
21	1882.5	39.3	942	11	Q8BG22	Q8bg22 mus musculu
22	1446	30.2	674	11	Q8BZF7	Q8bzf7 mus musculu
23	1326.5	27.7	513	11	Q91Z28	Q91z28 mus musculu
24	1050	21.9	337	11	Q8C9E1	Q8c9e1 mus musculu
25	987.5	20.6	342	6	O18744	O18744 bos taurus
26	741	15.5	262	4	Q9Y6N3	Q9y6n3 homo sapien
27	295	6.2	1004	17	Q8PU63	Q8pu63 methanosarc
28	220	4.6	109	6	Q29282	Q29282 sus scrofa
29	185	3.9	494	5	Q9U7P4	Q9u7p4 eufolliculi
30	177	3.7	1154	16	Q7U5X7	Q7u5x7 synechococc
31	174.5	3.6	589	17	Q8TU27	Q8tu27 methanosarc
32	173.5	3.6	842	16	Q897H0	Q897h0 clostridium
33	168	3.5	6310	16	Q88PP2	Q88pp2 pseudomonas
34	163	3.4	1450	16	Q9CE07	Q9ce07 lactococcus
35	161	3.4	1643	2	Q9F0P6	Q9f0p6 rickettsia
36	160	3.3	1386	16	Q92DL0	Q92dl0 listeria in
37	159.5	3.3	3624	16	Q8Z4I1	Q8z4i1 salmonella
38	159.5	3.3	3624	16	Q83SZ3	Q83sz3 salmonella
39	159	3.3	906	17	Q8TPY9	Q8tpy9 methanosarc
40	156.5	3.3	589	10	Q8LQ58	Q8lq58 oryza sativ
41	156	3.3	1270	3	Q9Y743	Q9y743 candida alb
42	155.5	3.2	3283	16	Q8Z1S2	Q8z1s2 salmonella
43	154	3.2	1086	5	O18428	O18428 geodia cydo
44	153.5	3.2	650	10	Q84WA3	Q84wa3 arabidopsis
45	153.5	3.2	676	10	Q9M1S2	Q9m1s2 arabidopsis

ALIGNMENTS

RESULT 1
Q9UNF7
ID Q9UNF7 PRELIMINARY; PRT; 917 AA.
AC Q9UNF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium-activated chloride channel protein 2.
GN CACC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=99364503; PubMed=10437792;
RA Agnel M., Vermat T., Culouscou J.M.;
RT "Identification of three novel members of the calcium-dependent
RT chloride channel (CaCC) family predominantly expressed in the
RT digestive tract and trachea.";
RL FEBS Lett. 455:295-301(1999).
DR EMBL; AF127035; AAD48398.1; -.
DR Genew; HGNC:2018; CLCA4.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR004727; CaCC_prot1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR00868; hCaCC; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 917 AA; 101153 MW; EA01090D781BEB95 CRC64;

Query Match 99.4%; Score 4763; DB 4; Length 917;
Best Local Similarity 99.7%; Pred. No. 2.1e-295;
Matches 916; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 MGLFRGFVFLLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTAS 60

```
Db          1 MGLFRGFVFLLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTAS 60

Qy         61 TYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQ 120

Qy        121 FTECGEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FTECGEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSK 180

Qy        181 KIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFM 240

Qy        241 QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLL 300

Qy        301 KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKLI 360
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KIRQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKLI 360

Qy        361 QIKSSDERNTLMAGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTAS 420
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Qy        421 SCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGN 480
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Qy        481 TDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIM 540
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Db        481 TDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIM 540

Qy        541 ENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM 600
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Db        541 ENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM 600

Qy        601 NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGV 660

Qy        661 YSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEID 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 YSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEID 720

Qy        721 EDTQTTLEDFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIILTWTAPGDN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATH 840
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Qy        841 IFIAIKSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL 900
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Qy        901 VLSVIGSVVIVNFILSTTI 919
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Db        899 VLSVIGSVVIVNFILSTTI 917
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RESULT 2
Q9UPC6
ID   Q9UPC6       PRELIMINARY;      PRT;   914 AA.
AC   Q9UPC6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Calcium-dependent chloride channel-1.
GN   CLCA1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99047526; PubMed=9828122;
RA   Gruber A.D., Elble R.C., Ji H.L., Schreur K.D., Fuller C.M.,
RA   Pauli B.U.;
RT   "Genomic cloning, molecular characterization, and functional analysis
RT   of human CLCA1, the first human member of the family of Ca2+-activated
RT   Cl- channel proteins.";
RL   Genomics 54:200-214(1998).
DR   EMBL; AF039401; AAC95429.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR   GO; GO:0006821; P:chloride transport; IEA.
DR   GO; GO:0015992; P:proton transport; IEA.
DR   InterPro; IPR000131; ATPase_gamma.
DR   InterPro; IPR004727; CaCC_prot1.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF00092; vwa; 1.
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DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   914 AA;  100160 MW;  7761362B66752AA3 CRC64;

  Query Match           60.2%;  Score 2884.5;  DB 4;  Length 914;
  Best Local Similarity 61.7%;  Pred. No. 2e-175;
  Matches  564;  Conservative  124;  Mismatches  215;  Indels   11;  Gaps    8;

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Db          1 MGPFKSSVFILILHLLEGALSNSLIQLNNNGYEGIVVAIDPNVPEDETLIQQIKDMVTQA 60

Qy         60 STYLFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTK 119
              | |||||| |||:||||:||||| ||    | ||| | :|:|||:||  | || |||||:
Db         61 SLYLFEATGKRFYFKNVAILIPETWKTKADYVRPKLETYKNADVLVAESTPPGNDEPYTE 120

Qy        120 QFTECGEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKS 179
              |   |||||| || ||| : |||  |||| || ||||||||||||||||| |: || :
Db        121 QMGNCGEKGERIHLTPDFIAGKKLAEYGPQGKAFVHEWAHLRWGVFDEYNNDEKFYLSNG 180

Qy        180 KKIEATRCSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMF 239
              :|:| ||||||:| | | ||||||| :: |  :  | || | |:|     |||||||||
Db        181 -RIQAVRCSAGITGTNVVKKCQGGSCYTKRCTFNKVTGLYEKGCEFVLQSRQTEKASIMF 239

Qy        240 MQSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSL 299
              | :||:|||| |: ||:|||: || ||| |||||||  :|||| | || | || | |||
Db        240 AQHVDSIVEFCTEQNHNKEAPNKQNQKCNLRSTWEVIRDSEDFKKTTPMTTQPPNPTFSL 299

Qy        300 LKISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLLQTVENGSWVGMVHFDSTATIVNKL 359
              |:| |||||||||||||    :||||:||| : ||||||| ||||||| ||| | : ::|
Db        300 LQIGQRIVCLVLDKSGSMATGNRLNRLNQAGQLFLLQTVELGSWVGMVTFDSAAHVQSEL 359

Qy        360 IQIKSSDERNTLMAGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTA 419
              ||| |  :|:||   ||   ||||||||:: || || : :   ||||::|||||||||
Db        360 IQINSGSDRDTLAKRLPAAASGGTSICSGLRSAFTVIRKKY-PTDGSEIVLLTDGEDNTI 418

Qy        420 SSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSG 479
              | | :|||||||||:| :||| :| : : |:||:|||    | ||: |||||||||||:||
Db        419 SGCFNEVKQSGAIIHTVALGPSAAQELEELSKMTGGLQTYASDQVQNNGLIDAFGALSSG 478

Qy        480 NTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTI 539
              |  :||:|:||||||||| :: ||| |||:|||||||| ||||| : || | |||||||
Db        479 NGAVSQRSIQLESKGLTLQNSQWMNGTVIVDSTVGKDTLFLITWTTQPPQILLWDPSGQK 538

Qy        540 MENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAK 599
              | ||  :||||| ||| |||||| |:||| :  :|||:|||||:|:::||||| :|
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Qy        600 MNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDG 659
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2004, 04:46:55 ; Search time 168 Seconds
(without alignments)
3035.714 Million cell updates/sec

Title: US-10-063-579-70
Perfect score: 4791
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10063579/runat_26042004_141001_14321/app_query.fasta_1.1095
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Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4760	99.4	3043	4	US-09-049-698-16	Sequence 16, Appl
2	4760	99.4	3181	4	US-09-049-698-18	Sequence 18, Appl
3	2882.5	60.2	3007	4	US-09-193-562D-27	Sequence 27, Appl
4	2879.5	60.1	2745	4	US-09-623-624-5	Sequence 5, Appli
5	2681	56.0	2931	4	US-09-623-624-1	Sequence 1, Appli
6	2341.5	48.9	3317	4	US-09-193-562D-1	Sequence 1, Appli
7	2282	47.6	3022	4	US-09-193-562D-33	Sequence 33, Appl
8	2191.5	45.7	3418	4	US-09-193-562D-29	Sequence 29, Appl
9	1950.5	40.7	2970	4	US-09-193-562D-31	Sequence 31, Appl
10	1950.5	40.7	3190	4	US-09-623-624-3	Sequence 3, Appli
11	1950.5	40.7	3951	4	US-09-643-597-160	Sequence 160, App
12	1950.5	40.7	3951	4	US-09-480-884A-160	Sequence 160, App
13	1950.5	40.7	3951	4	US-09-542-615A-160	Sequence 160, App
14	1950.5	40.7	3951	4	US-09-606-421B-160	Sequence 160, App
15	1950.5	40.7	3951	4	US-09-221-107-160	Sequence 160, App
16	1950	40.7	2773	4	US-09-643-597-358	Sequence 358, App
17	1950	40.7	8031	4	US-09-643-597-254	Sequence 254, App
18	1950	40.7	8031	4	US-09-480-884A-254	Sequence 254, App
19	1950	40.7	8031	4	US-09-542-615A-254	Sequence 254, App
20	1950	40.7	8031	4	US-09-606-421B-254	Sequence 254, App
21	1927	40.2	2784	4	US-09-643-597-168	Sequence 168, App
22	1927	40.2	2784	4	US-09-480-884A-168	Sequence 168, App
23	1927	40.2	2784	4	US-09-542-615A-168	Sequence 168, App
24	1927	40.2	2784	4	US-09-606-421B-168	Sequence 168, App
25	1913	39.9	3156	4	US-09-919-172-86	Sequence 86, Appl
26	1685	35.2	1081	4	US-09-016-434-928	Sequence 928, App
27	1685	35.2	1399	4	US-09-049-698-17	Sequence 17, Appl
28	1482	30.9	1512	4	US-09-016-434-850	Sequence 850, App
29	1445.5	30.2	3362	4	US-09-643-597-167	Sequence 167, App
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31	1445.5	30.2	3362	4	US-09-542-615A-167	Sequence 167, App
32	1445.5	30.2	3362	4	US-09-606-421B-167	Sequence 167, App
33	1058	22.1	619	4	US-09-016-434-931	Sequence 931, App
C 34	888	18.5	618	3	US-09-385-982-24	Sequence 24, Appl
35	875.5	18.3	576	3	US-09-385-982-23	Sequence 23, Appl
36	747.5	15.6	595	3	US-09-385-982-25	Sequence 25, Appl
37	736.5	15.4	611	3	US-09-385-982-27	Sequence 27, Appl
38	698	14.6	878	1	US-08-469-667-8	Sequence 8, Appli
39	698	14.6	878	4	US-09-224-110-8	Sequence 8, Appli
40	698	14.6	878	5	PCT-US95-07289-8	Sequence 8, Appli
41	617	12.9	742	3	US-09-385-982-33	Sequence 33, Appl
42	492	10.3	313	4	US-09-049-698-10	Sequence 10, Appl
43	427	8.9	242	4	US-09-049-698-8	Sequence 8, Appli
44	411	8.6	241	4	US-09-049-698-7	Sequence 7, Appli
45	408	8.5	233	4	US-09-049-698-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-049-698-16
; Sequence 16, Application US/09049698
; Patent No. 6368792
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA A.
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
; TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; TITLE OF INVENTION: TRACT
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,856

; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6068.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3043 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-049-698-16

Alignment Scores:

Pred. No.:	0	Length:	3043
Score:	4760.00	Matches:	916
Percent Similarity:	99.67%	Conservative:	0
Best Local Similarity:	99.67%	Mismatches:	1
Query Match:	99.35%	Indels:	2
DB:	4	Gaps:	1

US-10-063-579-70 (1-919) x US-09-049-698-16 (1-3043)

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Qy         21 ThrSerPheIleLysLeuAsnAsnAsnGlyPheGluAspIleValIleValIleAspPro 40
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Qy         41 SerValProGluAspGluLysIleIleGluGlnIleGluAspMetValThrThrAlaSer 60
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Qy         61 ThrTyrLeuPheGluAlaThrGluLysArgPhePhePheLysAsnValSerIleLeuIle 80
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Qy        141 LysLysGlnAsnGluTyrGlyProProGlyLysLeuPheValHisGluTrpAlaHisLeu 160
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Qy        161 ArgTrpGlyValPheAspGluTyrAsnGluAspGlnProPheTyrArgAlaLysSerLys 180
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Qy        201 GlnGlyGlySerCysLeuSerArgAlaCysArgIleAspSerThrThrLysLeuTyrGly 220
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Db        614 CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACTGTATGGA 673

Qy        221 LysAspCysGlnPhePheProAspLysValGlnThrGluLysAlaSerIleMetPheMet 240
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Qy        241 GlnSerIleAspSerValValGluPheCysAsnGluLysThrHisAsnGlnGluAlaPro 260
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Db        734 CAAAGTATTGATTCTGTTGTTGAATTTTGTAACGAAAAAACCCATAATCAAGAAGCTCCA 793

Qy        261 SerLeuGlnAsnIleLysCysAsnPheArgSerThrTrpGluValIleSerAsnSerGlu 280
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Qy        281 AspPheLysAsnThrIleProMetValThrProProProProProValPheSerLeuLeu 300
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Qy        301 LysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySerMetGlyGlyLys 320
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Qy        321 AspArgLeuAsnArgMetAsnGlnAlaAlaLysHisPheLeuLeuGlnThrValGluAsn 340
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Qy        341 GlySerTrpValGlyMetValHisPheAspSerThrAlaThrIleValAsnLysLeuIle 360
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Db       1034 GGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAAATAAGCTAATC 1093

Qy        361 GlnIleLysSerSerAspGluArgAsnThrLeuMetAlaGlyLeuProThrTyrProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 CAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTG 1153

Qy        381 GlyGlyThrSerIleCysSerGlyIleLysTyrAlaPheGlnValIleGlyGluLeuHis 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 GGAGGAACTTCCATCTGCTCTGGAATTAAATATGCATTTCAGGTGATTGGAGAGCTACAT 1213

Qy        401 SerGlnLeuAspGlySerGluValLeuLeuLeuThrAspGlyGluAspAsnThrAlaSer 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 TCCCAACTCGATGGATCCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGT 1273

Qy        421 SerCysIleAspGluValLysGlnSerGlyAlaIleValHisPheIleAlaLeuGlyArg 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 TCTTGTATTGATGAAGTGAAACAAAGTGGGGCCATTGTTCATTTTATTGCTTTGGGAAGA 1333

Qy        441 AlaAlaAspGluAlaValIleGluMetSerLysIleThrGlyGlySerHisPheTyrVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 GCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTT 1393

Qy        461 SerAspGluAlaGlnAsnAsnGlyLeuIleAspAlaPheGlyAlaLeuThrSerGlyAsn 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAAT 1453

Qy        481 ThrAspLeuSerGlnLysSerLeuGlnLeuGluSerLysGlyLeuThrLeuAsnSerAsn 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 ACTGATCTCTCCCAGAAGTCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAAT 1513

Qy        501 AlaTrpMetAsnAspThrValIleIleAspSerThrValGlyLysAspThrPhePheLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 GCCTGGATGAACGACACTGTCATAATTGATAGTACAGTGGGAAAGGACACGTTCTTTCTC 1573

Qy        521 IleThrTrpAsnSerLeuProProSerIleSerLeuTrpAspProSerGlyThrIleMet 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1574 ATCACATGGAACAGTCTGCCTCCCAGTATTTCTCTCTGGGATCCCAGTGGAACAATAATG 1633

Qy        541 GluAsnPheThrValAspAlaThrSerLysMetAlaTyrLeuSerIleProGlyThrAla 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1634 GAAAATTTCACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCCAGGAACTGCA 1693

Qy        561 LysValGlyThrTrpAlaTyrAsnLeuGlnAlaLysAlaAsnProGluThrLeuThrIle 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 AAGGTGGGCACTTGGGCATACAATCTTCAAGCCAAAGCGAACCCAGAAACATTAACTATT 1753

Qy        581 ThrValThrSerArgAlaAlaAsnSerSerValProProIleThrValAsnAlaLysMet 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 ACAGTAACTTCTCGAGCAGCAAATTCTTCTGTGCCTCCAATCACAGTGAATGCTAAAATG 1813
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Qy        601 AsnLysAspValAsnSerPheProSerProMetIleValTyrAlaGluIleLeuGlnGly 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 AATAAGGACGTAAACAGTTTCCCCAGCCCAATGATTGTTTACGCAGAAATTCTACAAGGA 1873

Qy        621 TyrValProValLeuGlyAlaAsnValThrAlaPheIleGluSerGlnAsnGlyHisThr 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1874 TATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACA 1933

Qy        641 GluValLeuGluLeuLeuAspAsnGlyAlaGlyAlaAspSerPheLysAsnAspGlyVal 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 GAAGTTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTC 1993

Qy        661 TyrSerArgTyrPheThrAlaTyrThrGluAsnGlyArgTyrSerLeuLysValArgAla 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 TACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATATAGCTTAAAAGTTCGGGCT 2053

Qy        681 HisGlyGlyAlaAsnThrAlaArgLeuLysLeuArgProProLeuAsnArgAlaAlaTyr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 CATGGAGGAGCAAACACTGCCAGGCTAAAATTACGGCCTCCACTGAATAGAGCCGCGTAC 2113

Qy        701 IleProGlyTrpValValAsnGlyGluIleGluAlaAsnProProArgProGluIleAsp 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 ATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAACCCGCCAAGACCTGAAATTGAT 2173

Qy        721 GluAspThrGlnThrThrLeuGluAspPheSerArgThrAlaSerGlyGlyAlaPheVal 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2174 GAGGATACTCAGACCACCTTGGAGGATTTCAGCCGAACAGCATCCGGAGGTGCATTTGTG 2233

Qy        741 ValSerGlnValProSerLeuProLeuProAspGlnTyrProProSerGlnIleThrAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2234 GTATCACAAGTCCCAAGCCTTCCCTTGCCTGACCAATACCCACCAAGTCAAATCACAGAC 2293

Qy        761 LeuAspAlaThrValHisGluAspLysIleIleLeuThrTrpThrAlaProGlyAspAsn 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2294 CTTGATGCCACAGTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAGGAGATAAT 2353

Qy        781 PheAspValGlyLysValGlnArgTyrIleIleArgIleSerAlaSerIleLeuAspLeu 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2354 TTTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTTGATCTA 2413

Qy        801 ArgAspSerPheAspAspAlaLeuGlnValAsnThrThrAspLeuSerProLysGluAla 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2414 AGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCACCAAAGGAGGCC 2473

Qy        821 AsnSerLysGluSerPheAlaPheLysProGluAsnIleSerGluGluAsnAlaThrHis 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2474 AACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCAC 2533

Qy        841 IlePheIleAlaIleLysSerIleAspLysSerAsnLeuThrSerLysValSerAsnIle 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2534 ATATTTATTGCCATTAAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT 2593

Qy        861 AlaGlnValThrLeuPheIleProGlnAlaAsnProAspAspIleAspProThrProThr 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2594 GCACAAGTAACTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT------CCTACT 2647

Qy        881 ProThrProThrProThrProAspLysSerHisAsnSerGlyValAsnIleSerThrLeu 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2648 CCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTG 2707

Qy        901 ValLeuSerValIleGlySerValValIleValAsnPheIleLeuSerThrThrIle 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2708 GTATTGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACCATT 2764

RESULT 2
US-09-049-698-18
; Sequence 18, Application US/09049698
; Patent No. 6368792
;  GENERAL INFORMATION:
;    APPLICANT:  BILLING-MEDEL, PATRICIA A.
;    APPLICANT:  COHEN, MAURICE
;    APPLICANT:  COLPITTS, TRACEY L.
;    APPLICANT:  FRIEDMAN, PAULA N.
;    APPLICANT:  HAYDEN, MARK
;    APPLICANT:  KLASS, MICHAEL R.
;    APPLICANT:  ROBERTS-RAPP, LISA
;    APPLICANT:  RUSSELL, JOHN C.
;    APPLICANT:  STROUPE, STEPHEN D.
;    TITLE OF INVENTION:  REAGENTS AND METHODS FOR THE
;    TITLE OF INVENTION:  USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
;    TITLE OF INVENTION:  TRACT
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/049,698
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/828,856
;      FILING DATE:  31-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Becker, Cheryl L.
;      REGISTRATION NUMBER:  35,441
;      REFERENCE/DOCKET NUMBER:  6068.US.P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847/935-1729
;      TELEFAX:  847/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3181 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-049-698-18

Alignment Scores:
Pred. No.:                0                Length:          3181
Score:                    4760.00          Matches:         916
Percent Similarity:       99.67%           Conservative:    0
Best Local Similarity:    99.67%           Mismatches:      1
Query Match:              99.35%           Indels:          2
DB:                       4                Gaps:            1

US-10-063-579-70 (1-919) x US-09-049-698-18 (1-3181)

Qy          1 MetGlyLeuPheArgGlyPheValPheLeuLeuValLeuCysLeuLeuHisGlnSerAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 ATGGGGTTATTCAGAGGTTTTGTTTTCCTCTTAGTTCTGTGCCTGCTGCACCAGTCAAAT 84

Qy         21 ThrSerPheIleLysLeuAsnAsnAsnGlyPheGluAspIleValIleValIleAspPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 ACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCT 144

Qy         41 SerValProGluAspGluLysIleIleGluGlnIleGluAspMetValThrThrAlaSer 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCT 204

Qy         61 ThrTyrLeuPheGluAlaThrGluLysArgPhePhePheLysAsnValSerIleLeuIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACGTACCTGTTTGAAGCCACAGAAAAAAGATTTTTTTTCAAAAATGTATCTATATTAATT 264

Qy         81 ProGluAsnTrpLysGluAsnProGlnTyrLysArgProLysHisGluAsnHisLysHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        265 CCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATGAAAACCATAAACAT 324
Qy        101 AlaAspValIleValAlaProProThrLeuProGlyArgAspGluProTyrThrLysGln 120
Db        325 GCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAG 384
Qy        121 PheThrGluCysGlyGluLysGlyGluTyrIleHisPheThrProAspLeuLeuLeuGly 140
Db        385 TTCACAGAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCTGACCTTCTACTTGAA 444
Qy        141 LysLysGlnAsnGluTyrGlyProProGlyLysLeuPheValHisGluTrpAlaHisLeu 160
Db        445 AAAAAACAAAATGAATATGGACCACCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTC 504
Qy        161 ArgTrpGlyValPheAspGluTyrAsnGluAspGlnProPheTyrArgAlaLysSerLys 180
Db        505 CGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAGTCAAAA 564
Qy        181 LysIleGluAlaThrArgCysSerAlaGlyIleSerGlyArgAsnArgValTyrLysCys 200
Db        565 AAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT 624
Qy        201 GlnGlyGlySerCysLeuSerArgAlaCysArgIleAspSerThrThrLysLeuTyrGly 220
Db        625 CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACTGTATGGA 684
Qy        221 LysAspCysGlnPhePheProAspLysValGlnThrGluLysAlaSerIleMetPheMet 240
Db        685 AAAGATTGTCAATTCTTTCCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG 744
Qy        241 GlnSerIleAspSerValValGluPheCysAsnGluLysThrHisAsnGlnGluAlaPro 260
Db        745 CAAAGTATTGATTCTGTTGTTGAATTTTGTAACGAAAAAACCCATAATCAAGAAGCTCCA 804
Qy        261 SerLeuGlnAsnIleLysCysAsnPheArgSerThrTrpGluValIleSerAsnSerGlu 280
Db        805 AGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTCTGAG 864
Qy        281 AspPheLysAsnThrIleProMetValThrProProProProProValPheSerLeuLeu 300
Db        865 GATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTG 924
Qy        301 LysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySerMetGlyGlyLys 320
Db        925 AAGATCAGTCAAAGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAG 984
Qy        321 AspArgLeuAsnArgMetAsnGlnAlaAlaLysHisPheLeuLeuGlnThrValGluAsn 340
Db        985 GACCGCCTAAATCGAATGAATCAAGCAGCAAAACATTTCCTGCTGCAGACTGTTGAAAAT 1044
Qy        341 GlySerTrpValGlyMetValHisPheAspSerThrAlaThrIleValAsnLysLeuIle 360
Db       1045 GGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAAATAAGCTAATC 1104
Qy        361 GlnIleLysSerSerAspGluArgAsnThrLeuMetAlaGlyLeuProThrTyrProLeu 380
Db       1105 CAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTG 1164
Qy        381 GlyGlyThrSerIleCysSerGlyIleLysTyrAlaPheGlnValIleGlyGluLeuHis 400
Db       1165 GGAGGAACTTCCATCTGCTCTGGAATTAAATATGCATTTCAGGTGATTGGAGAGCTACAT 1224
Qy        401 SerGlnLeuAspGlySerGluValLeuLeuLeuThrAspGlyGluAspAsnThrAlaSer 420
Db       1225 TCCCAACTCGATGGATCCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGT 1284
Qy        421 SerCysIleAspGluValLysGlnSerGlyAlaIleValHisPheIleAlaLeuGlyArg 440
Db       1285 TCTTGTATTGATGAAGTGAAACAAAGTGGGGCCATTGTTCATTTTATTGCTTTGGGAAGA 1344
Qy        441 AlaAlaAspGluAlaValIleGluMetSerLysIleThrGlyGlySerHisPheTyrVal 460
Db       1345 GCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTT 1404

Qy        461 SerAspGluAlaGlnAsnAsnGlyLeuIleAspAlaPheGlyAlaLeuThrSerGlyAsn 480
Db       1405 TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAAT 1464
Qy        481 ThrAspLeuSerGlnLysSerLeuGlnLeuGluSerLysGlyLeuThrLeuAsnSerAsn 500
Db       1465 ACTGATCTCTCCCAGAAGTCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAAT 1524
Qy        501 AlaTrpMetAsnAspThrValIleIleAspSerThrValGlyLysAspThrPhePheLeu 520
Db       1525 GCCTGGATGAACGACACTGTCATAATTGATAGTACAGTGGGAAAGGACACGTTCTTTCTC 1584
Qy        521 IleThrTrpAsnSerLeuProProSerIleSerLeuTrpAspProSerGlyThrIleMet 540
Db       1585 ATCACATGGAACAGTCTGCCTCCCAGTATTTCTCTCTGGGATCCCAGTGGAACAATAATG 1644
Qy        541 GluAsnPheThrValAspAlaThrSerLysMetAlaTyrLeuSerIleProGlyThrAla 560
Db       1645 GAAAATTTCACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCCAGGAACTGCA 1704
Qy        561 LysValGlyThrTrpAlaTyrAsnLeuGlnAlaLysAlaAsnProGluThrLeuThrIle 580
Db       1705 AAGGTGGGCACTTGGGCATACAATCTTCAAGCCAAAGCGAACCCAGAAACATTAACTATT 1764
Qy        581 ThrValThrSerArgAlaAlaAsnSerSerValProProIleThrValAsnAlaLysMet 600
Db       1765 ACAGTAACTTCTCGAGCAGCAAATTCTTCTGTGCCTCCAATCACAGTGAATGCTAAAATG 1824
Qy        601 AsnLysAspValAsnSerPheProSerProMetIleValTyrAlaGluIleLeuGlnGly 620
Db       1825 AATAAGGACGTAAACAGTTTCCCCAGCCCAATGATTGTTTACGCAGAAATTCTACAAGGA 1884
Qy        621 TyrValProValLeuGlyAlaAsnValThrAlaPheIleGluSerGlnAsnGlyHisThr 640
Db       1885 TATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACA 1944
Qy        641 GluValLeuGluLeuLeuAspAsnGlyAlaGlyAlaAspSerPheLysAsnAspGlyVal 660
Db       1945 GAAGTTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTC 2004
Qy        661 TyrSerArgTyrPheThrAlaTyrThrGluAsnGlyArgTyrSerLeuLysValArgAla 680
Db       2005 TACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATATAGCTTAAAAGTTCGGGCT 2064
Qy        681 HisGlyGlyAlaAsnThrAlaArgLeuLysLeuArgProProLeuAsnArgAlaAlaTyr 700
Db       2065 CATGGAGGAGCAAACACTGCCAGGCTAAAATTACGGCCTCCACTGAATAGAGCCGCGTAC 2124
Qy        701 IleProGlyTrpValValAsnGlyGluIleGluAlaAsnProProArgProGluIleAsp 720
Db       2125 ATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAACCCGCCAAGACCTGAAATTGAT 2184
Qy        721 GluAspThrGlnThrThrLeuGluAspPheSerArgThrAlaSerGlyGlyAlaPheVal 740
Db       2185 GAGGATACTCAGACCACCTTGGAGGATTTCAGCCGAACAGCATCCGGAGGTGCATTTGTG 2244
Qy        741 ValSerGlnValProSerLeuProLeuProAspGlnTyrProProSerGlnIleThrAsp 760
Db       2245 GTATCACAAGTCCCAAGCCTTCCCTTGCCTGACCAATACCCACCAAGTCAAATCACAGAC 2304
Qy        761 LeuAspAlaThrValHisGluAspLysIleIleLeuThrTrpThrAlaProGlyAspAsn 780
Db       2305 CTTGATGCCACAGTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAGGAGATAAT 2364
Qy        781 PheAspValGlyLysValGlnArgTyrIleIleArgIleSerAlaSerIleLeuAspLeu 800
Db       2365 TTTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTTGATCTA 2424
Qy        801 ArgAspSerPheAspAspAlaLeuGlnValAsnThrThrAspLeuSerProLysGluAla 820
Db       2425 AGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCACCAAAGGAGGCC 2484
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Qy        821 AsnSerLysGluSerPheAlaPheLysProGluAsnIleSerGluGluAsnAlaThrHis 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2485 AACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCAC 2544

Qy        841 IlePheIleAlaIleLysSerIleAspLysSerAsnLeuThrSerLysValSerAsnIle 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2545 ATATTTATTGCCATTAAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT 2604

Qy        861 AlaGlnValThrLeuPheIleProGlnAlaAsnProAspAspIleAspProThrProThr 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2605 GCACAAGTAACTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT------CCTACT 2658

Qy        881 ProThrProThrProThrProAspLysSerHisAsnSerGlyValAsnIleSerThrLeu 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2659 CCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTG 2718

Qy        901 ValLeuSerValIleGlySerValValIleValAsnPheIleLeuSerThrThrIle 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2719 GTATTGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACCATT 2775
```

RESULT 3
US-09-193-562D-27
; Sequence 27, Application US/09193562D
; Patent No. 6309857
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-562D-27

Alignment Scores:

Pred. No.:	1.91e-301	Length:	3007
Score:	2882.50	Matches:	564
Percent Similarity:	75.16%	Conservative:	123
Best Local Similarity:	61.71%	Mismatches:	216
Query Match:	60.16%	Indels:	11
DB:	4	Gaps:	8

US-10-063-579-70 (1-919) x US-09-193-562D-27 (1-3007)

```
Qy          1 MetGlyLeuPheArgGlyPheValPheLeuLeuValLeuCysLeuLeuHisGlnSer--- 19
              ||||||   |||:::     ||||||:::|||:::|||   ||||||      :::
Db         47 ATGGGGCCATTTAAGAGTTCTGTGTTCATCTTGATTCTTCACCTTCTAGAAGGGGCCCTG 106

Qy         20 AsnThrSerPheIleLysLeuAsnAsnAsnGlyPheGluAspIleValIleValIleAsp 39
              :::   |||   |||:::||||||||||||||:::|||   ||||||:::   ||||||
Db        107 AGTAATTCACTCATTCAGCTGAACAACAATGGCTATGAAGGCATTGTCGTTGCAATCGAC 166

Qy         40 ProSerValProGluAspGluLysIleIleGluGlnIleGluAspMetValThrThrAla 59
              |||:::|||||||||||||||   :::|||:::||||||:::|||||||||||   |||
Db        167 CCCAATGTGCCAGAAGATGAAACACTCATTCAACAAATAAAGGACATGGTGACCCAGGCA 226

Qy         60 SerThrTyrLeuPheGluAlaThrGluLysArgPhePhePheLysAsnValSerIleLeu 79
              |||   ||||||||||||||||||   |||||||||:::|||||||||||||:::||||||
Db        227 TCTCTGTATCTGTTTGAAGCTACAGGAAAGCGATTTTATTTCAAAAATGTTGCCATTTTG 286

Qy         80 IleProGluAsnTrpLysGluAsnProGlnTyrLysArgProLysHisGluAsnHisLys 99
              |||||||||   ||||||                |||   ||||||||   |||   :::|||
Db        287 ATTCCTGAAACATGGAAGACAAAGGCTGACTATGTGAGACCAAAACTTGAGACCTACAAA 346

Qy        100 HisAlaAspValIleValAlaProProThrLeuProGlyArgAspGluProTyrThrLys 119
              :::||||||||:::||||||      |||   ||||||   ||||||||||||||:::
Db        347 AATGCTGATGTTCTGGTTGCTGAGTCTACTCCTCCAGGTAATGATGAACCCTACACTGAG 406

Qy        120 GlnPheThrGluCysGlyGluLysGlyGluTyrIleHisPheThrProAspLeuLeuLeu 139
              |||           ||||||||||||||||||   ||||||   |||||||||   :::
Db        407 CAGATGGGCAACTGTGGAGAGAAGGGTGAAAGGATCCACCTCACTCCTGATTTCATTGCA 466

Qy        140 GlyLysLysGlnAsnGluTyrGlyProProGlyLysLeuPheValHisGluTrpAlaHis 159
              |||||||||      ||||||||||||   ||||||   ||||||||||||||||||||
Db        467 GGAAAAAAGTTAGCTGAATATGGACCACAAGGTAAGGCATTTGTCCATGAGTGGGCTCAT 526

Qy        160 LeuArgTrpGlyValPheAspGluTyrAsnGluAspGlnProPheTyrArgAlaLysSer 179
              ||||||||||||||||||||||||||||||||   |||:::   ||||||   :::
Db        527 CTACGATGGGGAGTATTTGACGAGTACAATAATGATGAGAAATTCTACTTATCCAATGGA 586

Qy        180 LysLysIleGluAlaThrArgCysSerAlaGlyIleSerGlyArgAsnArgValTyrLys 199
                 :::|||:::|||   ||||||||||||||||||:::|||   |||   |||   |||
Db        587 ---AGAATACAAGCAGTAAGATGTTCAGCAGGTATTACTGGTACAAATGTAGTAAAGAAG 643

Qy        200 CysGlnGlyGlySerCysLeuSerArgAlaCysArgIleAspSerThrThrLysLeuTyr 219
              ||||||||||||||||||   ::::::   |||       :::       |||   ||||||
Db        644 TGTCAGGGAGGCAGCTGTTACACCAAAAGATGCACATTCAATAAAGTTACAGGACTCTAT 703

Qy        220 GlyLysAspCysGlnPhePheProAspLysValGlnThrGluLysAlaSerIleMetPhe 239
                 |||   |||:::|||                |||||||||||||||||||||||||
Db        704 GAAAAAGGATGTGAGTTTGTTCTCCAATCCCGCCAGACGGAGAAGGCTTCTATAATGTTT 763

Qy        240 MetGlnSerIleAspSerValValGluPheCysAsnGluLysThrHisAsnGlnGluAla 259
                 |||   :::||||||:::|||||||||||||   |||:::   ||||||:::||||||
Db        764 GCACAACATGTTGATTCTATAGTTGAATTCTGTACAGAACAAAACCACAACAAAGAAGCT 823

Qy        260 ProSerLeuGlnAsnIleLysCysAsnPheArgSerThrTrpGluValIleSerAsnSer 279
              |||:::   ||||||   |||||||||   |||||||||||||||||||   :::|||
Db        824 CCAAACAAGCAAAATCAAAAATGCAATCTCCGAAGCACATGGGAAGTGATCCGTGATTCT 883

Qy        280 GluAspPheLysAsnThrIleProMetValThrProProProProProValPheSerLeu 299
              ||||||||||||   |||   ||||||   |||   ||||||   |||   |||||||||
Db        884 GAGGACTTTAAGAAAACCACTCCTATGACAACACAGCCACCAAATCCCACCTTCTCATTG 943

Qy        300 LeuLysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySerMetGlyGly 319
              |||:::|||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        944 CTGCAGATTGGACAAAGAATTGTGTGTTTAGTCCTTGACAAATCTGGAAGCATGGCGACT 1003

Qy        320 LysAspArgLeuAsnArgMetAsnGlnAlaAlaLysHisPheLeuLeuGlnThrValGlu 339
                 :::|||||||||||:::|||||||||   :::   ||||||||||||||||||||||
Db       1004 GGTAACCGCCTCAATCGACTGAATCAAGCAGGCCAGCTTTTCCTGCTGCAGACAGTTGAG 1063

Qy        340 AsnGlySerTrpValGlyMetValHisPheAspSerThrAlaThrIleValAsnLysLeu 359
                 ||||||||||||||||||   |||||||||   |||   :::   .::::::|||
Db       1064 CTGGGGTCCTGGGTTGGGATGGTGACATTTGACAGTGCTGCCCATGTACAAAGTGAACTC 1123

Qy        360 IleGlnIleLysSerSerAspGluArgAsnThrLeuMetAlaGlyLeuProThrTyrPro 379
              |||||||||   |||       :::|||:::||||||         ||||||
Db       1124 ATACAGATAAACAGTGGCAGTGACAGGGACACACTCGCCAAAAGATTACCTGCAGCAGCT 1183

Qy        380 LeuGlyGlyThrSerIleCysSerGlyIleLysTyrAlaPheGlnValIleGlyGluLeu 399
                 |||||||||||||||||||||||:::::::   ||||||   ||||||   :::
Db       1184 TCAGGAGGGACGTCCATCTGCAGCGGGCTTCGATCGGCATTTACTGTGATTAGGAAGAAA 1243

Qy        400 HisSerGlnLeuAspGlySerGluValLeuLeuLeuThrAspGlyGluAspAsnThrAla 419
                 :::         ||||||||||||:::::::||||||||||||||||||||||||
Db       1244 TAT---CCAACTGATGGATCTGAAATTGTGCTGCTGACGGATGGGGAAGACAACACTATA 1300

Qy        420 SerSerCysIleAspGluValLysGlnSerGlyAlaIleValHisPheIleAlaLeuGly 439
                 |||   |||   :::|||||||||||||||||||||||||||:::|||   :::||||||
Db       1301 AGTGGGTGCTTTAACGAGGTCAAACAAAGTGGTGCCATCATCCACACAGTCGCTTTGGGG 1360

Qy        440 ArgAlaAlaAspGluAlaValIleGluMetSerLysIleThrGlyGlySerHisPheTyr 459
                 :::|||   :::   :::   |||:::||||||:::|||||||||          |||
Db       1361 CCCTCTGCAGCTCAAGAACTAGAGGAGCTGTCCAAAATGACAGGAGGTTTACAGACATAT 1420

Qy        460 ValSerAspGluAlaGlnAsnAsnGlyLeuIleAspAlaPheGlyAlaLeuThrSerGly 479
              ||||||:::   |||||||||||||||||||||||||||||||||||:::||||||
Db       1421 GCTTCAGATCAAGTTCAGAACAATGGCCTCATTGATGCTTTTGGGGCCCTTTCATCAGGA 1480
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